

SEQUENCE LISTING

<110> Benjanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US5.DIV

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<141> 2001-11-13

<150> US 09/924,340

<151> 2001-08-06

<150> PCT/IB01/01715

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1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl *a* is located in the thylakoid membranes of chloroplasts.

2. *Chlorophyll b* (Chl *b*) is an accessory pigment that absorbs light energy in the blue and orange-yellow regions of the visible spectrum. It transfers the absorbed energy to Chl *a*. Chl *b* is also located in the thylakoid membranes.

3. *Carotenoids* are a group of pigments that absorb light energy in the blue and green regions of the visible spectrum. They include carotenes (orange) and xanthophylls (yellow). Carotenoids transfer energy to Chl *a* and also protect the photosynthetic apparatus from damage by excess light.

4. *Xanthophylls* are a subset of carotenoids that absorb light energy in the blue and green regions. They play a role in photoprotection and energy transfer.

5. *Phycocyanin* is a blue pigment found in cyanobacteria and some algae. It absorbs light energy in the orange and red regions and transfers it to Chl *a*.

6. *Peridinin* is an orange pigment found in certain dinoflagellates. It absorbs light energy in the blue and green regions and transfers it to Chl *a*.

7. *Alloxanthin* is a yellow pigment found in some algae. It absorbs light energy in the blue and green regions and transfers it to Chl *a*.

8. *Diatoxanthin* is a yellow pigment found in diatoms. It absorbs light energy in the blue and green regions and transfers it to Chl *a*.

9. *Diadinoxanthin* is a yellow pigment found in diatoms. It absorbs light energy in the blue and green regions and transfers it to Chl *a*.

10. *Zeaxanthin* is a yellow pigment found in many plants and algae. It absorbs light energy in the blue and green regions and transfers it to Chl *a*. It is also involved in the xanthophyll cycle for photoprotection.

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gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
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Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
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Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
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Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
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Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
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Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
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Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
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Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
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Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
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 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
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 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
 65 70 75
 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
 80 85 90 95
 Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
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 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
 115 120 125
 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
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 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
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 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
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 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp
 15 20 25
 tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act 312
 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr
 30 35 40

<221> 3'UTR
<222> 1213..1746

<220>
<221> polyA_signal
<222> 1709..1714

<220>
<221> polyA_site
<222> 1733..1746

<400> 23
gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt 51
Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys
-15 -10 -5
tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg 99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
1 5 10
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Leu Gly Thr Asp Leu Val
15 20 25 30
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
35 40 45
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
50 55 60
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
65 70 75
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
80 85 90
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
95 100 105 110
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
115 120 125
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
130 135 140
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
145 150 155
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
160 165 170
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc 627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
175 180 185 190
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
195 200 205
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg 723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
210 215 220
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac 771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
225 230 235
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
240 245 250

<220>
 <221> UNSURE
 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

<400> 28
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 1 5 10 15
 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
 20 25 30
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
 85 90 95
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
 100 105 110
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
 115 120 125
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
 130 135 140
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
 145 150 155 160
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
 165 170 175
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 180 185 190
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 195 200 205
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 210 215 220
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 225 230 235 240
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 245 250 255
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 260 265 270
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280

<210> 29
 <211> 1118
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..344

<220>
 <221> CDS
 <222> 345..1118

<220>
 <221> polyA_site

<222> 1103..1118

<400> 29

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tgtggcctgg ggaagagg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120
tggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180
aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
cggcccgag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
Met Gly Arg Thr
cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
-15 -10 -5 1
tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
5 10 15
atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
20 25 30
gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
35 40 45
aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
50 55 60 65
gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
70 75 80
gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
85 90 95
gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
100 105 110
tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
115 120 125
ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
130 135 140 145
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
150 155 160
cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
165 170 175
aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
180 185 190
atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
195 200 205
act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
Thr Leu Gly Asn Asn Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
210 215 220 225
gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa aaa 1118
Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys
230 235

<210> 30

<211> 258

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>
 <221> UNSURE
 <222> 49
 <223> Xaa = Glu, *

<400> 30
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 -20 -15 -10 -5
 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp
 1 5 10
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
 15 20 25
 Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
 30 35 40
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
 45 50 55 60
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
 65 70 75
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
 80 85 90
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
 95 100 105
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
 110 115 120
 Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
 125 130 135 140
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
 145 150 155
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
 160 165 170
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
 175 180 185
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
 190 195 200
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
 205 210 215 220
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
 225 230 235
 Lys Lys

<210> 31
 <211> 1273
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..13

<220>
 <221> CDS
 <222> 14..1048

<220>
 <221> 3'UTR
 <222> 1049..1273

<220>

<221> polyA_signal

<222> 1234..1239

<220>

<221> polyA_site

<222> 1258..1273

<400> 31

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      Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
      -25                                -20                                -15
tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
      -10                                -5                                1
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac      145
Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
      5                                10                                15
ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt      193
Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val
      20                                25                                30                                35
gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga      241
Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg
      40                                45                                50
agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc      289
Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro
      55                                60                                65
tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt      337
Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe
      70                                75                                80
aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg      385
Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu
      85                                90                                95
aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg      433
Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu
      100                                105                                110                                115
gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac      481
Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn
      120                                125                                130
aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att      529
Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
      135                                140                                145
ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg      577
Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
      150                                155                                160
cag cgg aca atg atc aga tat ttc aca tgc aat cca gcc tca aag gtc      625
Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
      165                                170                                175
ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt      673
Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
      180                                185                                190                                195
cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata      721
His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile
      200                                205                                210
gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca      769
Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala
      215                                220                                225
ggt gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga      817
Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly
      230                                235                                240
aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg      865
Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met
      245                                250                                255
gat aca gca gga atg atc ctg gga tgg aaa ttt ttt gat cat gcg gca      913
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265 270 275
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..72

<220>
 <221> CDS
 <222> 73..672

<220>
 <221> 3'UTR
 <222> 673..723

<220>
 <221> polyA_signal
 <222> 689..694

<220>
 <221> polyA_site
 <222> 708..723

<400> 33
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 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
 110 115 120 125
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Thr Phe Gly Phe Ile Leu
 130 135 140
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543

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Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
      145                      150                      155
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
      160                      165                      170
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
      175                      180                      185
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
      190                      195                      200
aagatgtgtt aaaataaaaa aaaaaaaaaa t 723

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<210> 34
<211> 200
<212> PRT
<213> Homo sapiens

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<400> 34
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
1      5      10      15
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
      20      25      30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
      35      40      45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
      50      55      60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
65      70      75      80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
      85      90      95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
      100     105     110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
      115     120     125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
      130     135     140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
145     150     155     160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
      165     170     175
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
      180     185     190
Asp Cys Asp Cys Glu Gln Cys Cys
      195     200

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<210> 35
<211> 845
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..118

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<220>
<221> CDS
<222> 119..655

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<220>
<221> 3'UTR
<222> 656..845

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<220>
 <221> polyA_signal
 <222> 809..814

<220>
 <221> polyA_site
 <222> 830..845

<400> 35
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 taaattctgc caaaaggact gaggaacggg gcctggaaaaa gggcaagaat atcacggc 118
 atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
 1 5 10 15
 aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
 Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
 20 25 30
 tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60
 gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
 Leu Leu Met Ser Phe Phe Ile Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
 Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
 100 105 110
 atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
 Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
 115 120 125
 atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
 Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
 130 135 140
 acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
 Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
 145 150 155 160
 tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
 Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
 165 170 175
 ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
 Gly Pro Tyr
 atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggg 755
 attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815
 cagtttatta tcgcaaaaaa aaaaaaaaaa 845

<210> 36
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
 1 5 10 15
 Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
 20 25 30
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met

<400> 38
 Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
 1 5 10 15
 Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
 20 25 30
 Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
 35 40 45
 Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
 50 55 60
 Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
 65 70 75 80
 Ala

<210> 39
 <211> 1816
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..259

<220>
 <221> CDS
 <222> 260..1048

<220>
 <221> 3'UTR
 <222> 1049..1816

<220>
 <221> polyA_signal
 <222> 1782..1787

<220>
 <221> polyA_site
 <222> 1801..1816

<400> 39
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 ggaacctcgg gaggcgagc tccggcgccct ggtagcgaga ggcgggttcc ggagatcccc 120
 gcctcacttc gtcccactgt ggtaggggt gagtctcgcg aatgttaagt gatttgctca 180
 aggtgcccac ttgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
 -15 -10
 ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
 -5 1 5
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
 10 15 20
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
 25 30 35 40
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tgc tgg gtg ggg ccc 484
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro
 45 50 55
 aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
 Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
 60 70
 gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
 Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His

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      75      80      85
gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc 628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
      90      95     100
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc 676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
105      110     115     120
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc 724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
      125      130     135
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc 772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
      140      145     150
att tgc ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc 820
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr
155      160     165
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc 868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
170      175     180
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg 916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu
185      190     195     200
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag 964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
205      210     215
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac 1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
220      225     230
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgtc 1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
235      240
tcccaagaac agagcctgtc ccagatgtc ccagtagcga tgagtaacag aggtggctgt 1118
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gaagcctggg gtttggagcc cacctactct ctggcagcat cagcatccta ctccctggcaa 1598
catcaggcca acgtccaccc cagcctcaca ttgccagatg ttggcagaag ggctaattatt 1658
gaccgtcttg actggctgga gccttcaaag ccactgggat gtccctccagg cacctgggtc 1718
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<210> 40
 <211> 263
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..20

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 Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg
 1 5 10
 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
 15 20 25
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
 30 35 40


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gct gac cag aac tgc acg caa gag tgc gtc tgc gac agc gaa tgc gcc 258
Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
      15                20                25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
      30                35                40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
      45                50                55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
      60                65                70                75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
      80                85                90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
      95
agttttctgcc tggccctgca tctgggtcca gccacctgc cctccccttt ttcgggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

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<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..30

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<400> 42
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Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
      -10                -5                1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
      5                10                15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
      20                25                30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
      35                40                45                50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
      55                60                65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
      70                75                80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
      85                90

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<210> 43
<211> 501
<212> DNA
<213> Homo sapiens

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<220>
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<222> 1..227

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<220>
<221> CDS
<222> 228..501

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<400> 43

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 agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
 ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
 ccattggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
 Met Gln Gly
 -30
 act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
 Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
 -25 -20 -15
 aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
 Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
 -10 -5 1
 aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
 Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
 5 10 15
 cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
 Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
 20 25 30 35
 gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
 Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
 40 45 50
 gtt cct ttc tcc gaa ctg aaa gac a 501
 Val Pro Phe Ser Glu Leu Lys Asp
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<210> 44
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..33

<400> 44
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 Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
 -15 -10 -5
 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
 1 5 10 15
 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
 20 25 30
 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
 35 40 45
 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
 50 55

<210> 45
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 <212> DNA
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 <222> 98..934

<220>
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<222> 935..960

<400> 45

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cggcccgttt caccgccagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
Met Thr Pro Ser Glu Gly
1 5
gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
10 15 20
gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
25 30 35
cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259
Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
40 45 50
caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
55 60 65 70
ggg ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
75 80 85
aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
90 95 100
ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
105 110 115
gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro
120 125 130
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
135 140 145 150
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
Cys Pro Gly Asp Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
155 160 165
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
170 175 180
ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
185 190 195
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr
200 205 210
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly
215 220 225 230
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta 835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Val
235 240 245
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt 883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly
250 255 260
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga 931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly
265 270 275
ttc tagggatggg gcagagtggc agcatc 960
Phe

<210> 46

<211> 279

<212> PRT
<213> Homo sapiens

<400> 46

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Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val Leu Leu Arg Asp
20 25 30
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
35 40 45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
50 55 60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
65 70 75 80
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
85 90 95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
100 105 110
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
115 120 125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
130 135 140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys
145 150 155 160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
165 170 175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
180 185 190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
195 200 205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
210 215 220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
225 230 235 240
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
245 250 255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
260 265 270
Trp Gly Trp Gly Gln Gly Phe
275

<210> 47
<211> 1294
<212> DNA
<213> Homo sapiens

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<222> 1140..1294

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<222> 1246..1251

<220>

Ala Tyr Glu Glu Ile Phe Val Lys Asn Met

255

260

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ctaaaatgct ttttaattaat atgttcatta aattttctat gcttattgta cttgttacca 1279

aaaaaaaaa aaaaa

1294

<210> 48

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..28

<400> 48

Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys

-25

-20

-15

Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu

-10

-5

1

Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys

5

10

15

20

Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys

25

30

35

Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu

40

45

50

Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser

55

60

65

Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys

70

75

80

Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr

85

90

95

100

Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly

105

110

115

Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn

120

125

130

Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr

135

140

145

Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val

150

155

160

Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala

165

170

175

180

Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser

185

190

195

Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn

200

205

210

Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys

215

220

225

Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg

230

235

240

Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val

245

250

255

260

Lys Asn Met

<210> 49

<211> 1194

<212> DNA

<213> Homo sapiens

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<220>
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 <222> 1159..1164

<220>
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 <222> 1179..1194

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 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152
 Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
 1 5 10
 ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200
 Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
 15 20 25
 ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
 Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
 30 35 40
 cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296
 Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
 45 50 55 60
 gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344
 Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
 65 70 75
 ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392
 Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
 80 85 90
 gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440
 Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
 95 100 105
 gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488
 Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
 110 115 120
 aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536
 Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
 125 130 135 140
 gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584
 Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
 145 150 155
 cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632
 Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
 160 165 170
 gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680
 Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
 175 180 185
 cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728
 Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
 190 195 200
 atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776
 Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu

Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser
 205 210 215
 Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu
 220 225 230
 Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly
 235 240 245
 Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
 250 255 260
 Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala
 265 270 275 280
 Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu
 285 290 295
 Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr
 300 305 310
 Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys
 315 320 325

<210> 51
 <211> 1317
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..289

<220>
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 <222> 290..1162

<220>
 <221> 3'UTR
 <222> 1163..1317

<220>
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 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1302..1317

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 gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180
 aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact 240
 ccgttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac 298
 Met Ile Tyr
 -25
 aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346
 Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu
 -20 -15 -10
 aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa 394
 Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu
 -5 1 5
 cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat 442
 His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His
 10 15 20
 tca ttt tgt gca ttc aag tcg gat gat ggc cca tgt aaa gca atc atg 490
 Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys Ala Ile Met
 25 30 35 40
 aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata 538

Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile
 45 50 55
 tat ggg gga tgt gaa gga aat cag aat cga ttt gaa agt ctg gaa gag 586
 Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu
 60 65 70
 tgc aaa aaa atg tgt aca aga gaa aag cca gat ttc tgc ttt ttg gaa 634
 Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu
 75 80 85
 gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat aac 682
 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
 90 95 100
 aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga tgc ctg ggc 730
 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
 105 110 115 120
 aat atg aac aat ttt gag aca ctg gaa gaa tgc aag aac att tgt gaa 778
 Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu
 125 130 135
 gat ggt ccg aat ggt ttc cag gtg gat aat tat gga acc cag ctc aat 826
 Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn
 140 145 150
 gct gtg aat aac tcc ctg act ccg caa tca acc aag gtt ccc agc ctt 874
 Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu
 155 160 165
 ttt gaa ttt cac ggt ccc tca tgg tgt ctc act cca gca gac aga gga 922
 Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly
 170 175 180
 ttg tgt cgt gcc aat gag aac aga ttc tac tac aat tca gtc att ggg 970
 Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly
 185 190 195 200
 aaa tgc cgc cca ttt aag tac agt gga tgt ggg gga aat gaa aac aat 1018
 Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn
 205 210 215
 ttt act tcc aaa caa gaa tgt ctg agg gca tgt aaa aaa ggt ttc atc 1066
 Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile
 220 225 230
 caa aga ata tca aaa gga ggc cta att aaa acc aaa aga aaa aga aag 1114
 Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys
 235 240 245
 aag cag aga gtg aaa ata gca tat gaa gaa att ttt gtt aaa aat atg 1162
 Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
 250 255 260
 tgaatttggt atagcaatgt aacattaatt ctactaaata ttttatatga aatgtttcac 1222
 tatgattttc tatttttctt ctaaaatgct tttaattaat atgttcatta aattttctat 1282
 gcttattgta cttgttatca aaaaaaaaaa aaaaa 1317

<210> 52
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400> 52
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
 -25 -20 -15
 Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
 25 30 35

180 185 190
 Ser Phe Arg Ile His Phe Trp Gly Cys
 195 200

<210> 57
 <211> 1133
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..475

<220>
 <221> CDS
 <222> 476..964

<220>
 <221> 3'UTR
 <222> 965..1133

<220>
 <221> polyA_signal
 <222> 1101..1106

<220>
 <221> polyA_site
 <222> 1118..1133

<400> 57
 gacataatca gagctatgct ggaggagaag agggcagcca ttgctggct ggcttgcaagt 60
 gagccaggag gtggcaggac gagttaggag gctggttcag tagctcgggc aagagcaggg 120
 cccccagga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg 180
 aggaccccaa ggtaactccg gtgagaaggg cgaccaggga tttcaaggcc agccaggctt 240
 tccgggccc cccgggtcccc ctggattccc aggcaaagtt ggatcacctg gcccacctgg 300
 cctcaagca gagaagggca gcgaagggat tcgaggccca tcaggcctgc ctgggtcccc 360
 tgggccaccg ggacctcctg ggattcaggg ccccgccggg ctggatggtt tggatgggaa 420
 ggatggcaag cctggcttga ggggggaccc tggctcctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
 50 55 60 65
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
 70 75 80
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
 85 90 95
 cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
 Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
 100 105 110
 ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
 Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly

```

      115              120              125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
130              135              140              145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
      150              155              160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacagggtg tgaatgtttt tttgttggtt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaaa 1133

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<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

```

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<400> 58
Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro
1              5              10              15
Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
      20              25              30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
      35              40              45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
      50              55              60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
      65              70              75              80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
      85              90              95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
      100              105              110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
      115              120              125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
      130              135              140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
      145              150              155              160
Pro Phe Gly

```

```

<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..78

```

```

<220>
<221> CDS
<222> 79..642

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```

<220>
<221> 3'UTR
<222> 643..838

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<220>
<221> polyA_signal
<222> 799..804

```

```

<220>
<221> polyA_site

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<222> 823..838

<400> 59

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aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggtc 60
cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
      Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
      1          5          10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
      15          20          25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
      30          35          40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
      45          50          55
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
      60          65          70          75
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
      80          85          90
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
      95          100          105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
      110          115          120
cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
      125          130          135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
      140          145          150          155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
      160          165          170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
      175          180          185
aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccaccct 692
Lys
gacctctccc tcagctgtcc tgtgccccgc cctctccccgc acactcagtc cccctgcctg 752
gcgttccctgc cgcagctctg acctggtgct gtcgccctgg catcttaata aamcctgctt 812
atatttcctt aaaaaaaaaa aaaaaa 838
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<210> 60

<211> 188

<212> PRT

<213> Homo sapiens

<400> 60

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Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1          5          10          15
Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
      20          25          30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
      35          40          45
Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
      50          55          60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
      65          70          75          80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
```



```

115              120              125              130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
              135              140              145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
              150              155              160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
              165              170              175
ttc ggg atc gtg tagccggcgg ggcggggggcc gtgggggggcc tggaggaggg 804
Phe Gly Ile Val
              180
caggagccgc gggaggccgg gaggagggtg gggaccttgc agcccccatc ctctccgt 862

```

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<210> 62
<211> 202
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..21

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<400> 62
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
-20 -15 -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
-5 1 5 10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
15 20 25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
30 35 40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
45 50 55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
60 65 70 75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
80 85 90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
95 100 105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
110 115 120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
125 130 135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
140 145 150 155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
160 165 170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
175 180

```

```

<210> 63
<211> 618
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..194

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<220>
<221> CDS

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<222> 195..587

<220>

<221> 3'UTR

<222> 588..618

<220>

<221> polyA_signal

<222> 578..583

<220>

<221> polyA_site

<222> 604..618

<400> 63

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atttgcttag gtctgatcaa tctgctccac acaatttctc agtgatcctc tgcattctctg 60
cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
ttcgttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180
acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
                Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
                -20                -15                -10
act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
                -5                1                5
cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
                10                15                20
agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
                25                30                35
tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
                40                45                50                55
aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
                60                65                70
atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
                75                80                85
act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
                90                95                100
tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
Cys Phe Ala Leu Leu Asn Cys
                105                110
```

<210> 64

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..22

<400> 64

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Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
                -20                -15                -10
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
                -5                1                5                10
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
                15                20                25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
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<222> 1..62

<220>

<221> CDS

<222> 63..572

<220>

<221> 3'UTR

<222> 573..789

<220>

<221> polyA_signal

<222> 750..755

<220>

<221> polyA_site

<222> 774..789

<400> 67

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atatgtcatc agggcccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggagggac gcccagggtg gggaggaaga gtctgcaagc agggctgtgg agttagggtt 652
caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
gaaaaaaaaa aaaaaaaa 789
```

<210> 68

<211> 170

<212> PRT

<213> Homo sapiens

ttg Leu	gag Glu	gga Gly	aat Asn	gaa Glu	atc Ile	tgt Cys	gat Asp	tgt Cys	ggt Gly	act Thr	gag Glu	gct Ala	caa Gln	tgt Cys	gga Gly	1308
385 390 395																
cct Pro	gca Ala	agc Ser	tgt Cys	tgt Cys	gat Asp	ttt Phe	cga Arg	act Thr	tgt Cys	gta Val	ctg Leu	aaa Lys	gac Asp	gga Gly	gca Ala	1356
400 405 410 415																
aaa Lys	tgt Cys	tat Tyr	aaa Lys	gga Gly	ctg Leu	tgc Cys	tgc Cys	aaa Lys	gac Asp	tgt Cys	caa Gln	att Ile	tta Leu	caa Gln	tca Ser	1404
420 425 430																
ggc Gly	gtt Val	gaa Glu	tgt Cys	agg Arg	ccg Pro	aaa Lys	gca Ala	cat His	cct Pro	gaa Glu	tgt Cys	gac Asp	atc Ile	gct Ala	gaa Glu	1452
435 440 445																
aat Asn	tgt Cys	aat Asn	gga Gly	agc Ser	tca Ser	cca Pro	gaa Glu	tgt Cys	ggt Gly	cct Pro	gac Asp	ata Ile	act Thr	tta Leu	atc Ile	1500
450 455 460																
aat Asn	gga Gly	ctt Leu	tca Ser	tgc Cys	aaa Lys	aat Asn	aat Asn	aag Lys	ttt Phe	att Ile	tgt Cys	tat Tyr	gac Asp	gga Gly	gac Asp	1548
465 470 475																
tgc Cys	cat His	gat Asp	ctc Leu	gat Asp	gca Ala	cgt Arg	tgt Cys	gag Glu	agt Ser	gta Val	ttt Phe	gga Gly	aaa Lys	ggt Gly	tca Ser	1596
480 485 490 495																
aga Arg	aat Asn	gct Ala	cca Pro	ttt Phe	gcc Ala	tgc Cys	tat Tyr	gaa Glu	gaa Glu	ata Ile	caa Gln	tct Ser	caa Gln	tca Ser	gac Asp	1644
500 505 510																
aga Arg	ttt Phe	ggg Gly	aac Asn	tgt Cys	ggt Gly	agg Arg	gat Asp	aga Arg	aat Asn	aac Asn	aaa Lys	tat Tyr	gtg Val	ttc Phe	tgt Cys	1692
515 520 525																
gga Gly	tgg Trp	agg Arg	aat Asn	ctt Leu	ata Ile	tgt Cys	gga Gly	aga Arg	tta Leu	gtt Val	tgt Cys	acc Thr	tac Tyr	cct Pro	act Thr	1740
530 535 540 545																
cga Arg	aag Lys	cct Pro	ttc Phe	cat His	caa Gln	gaa Glu	aat Asn	ggt Gly	gat Asp	gtg Val	att Ile	tat Tyr	gct Ala	ttc Phe	gta Val	1788
550 555																
cga Arg	gat Asp	tct Ser	gta Val	tgc Cys	ata Ile	acc Thr	gta Val	gac Asp	tac Tyr	aaa Lys	ttg Leu	cct Pro	cga Arg	aca Thr	gtt Val	1836
560 565 570 575																
cca Pro	gat Asp	cca Pro	ctg Leu	gct Ala	gtc Val	aaa Lys	aat Asn	ggc Gly	tct Ser	cag Gln	tgt Cys	gat Asp	att Ile	ggg Gly	agg Arg	1884
580 585 590																
gtt Val	tgt Cys	gta Val	aat Asn	cgt Arg	gaa Glu	tgt Cys	gta Val	gaa Glu	tca Ser	agg Arg	ata Ile	att Ile	aag Lys	gct Ala	tca Ser	1932
595 600 605																
gca Ala	cat His	gtt Val	tgt Cys	tca Ser	caa Gln	cag Gln	tgt Cys	tct Ser	gga Gly	cat His	gga Gly	gtg Val	tgt Cys	gat Asp	tcc Ser	1980
610 615 620																
aga Arg	aac Asn	aag Lys	tgc Cys	cat His	tgt Cys	tcg Ser	cca Pro	ggc Gly	tat Tyr	aag Lys	cct Pro	cca Pro	aac Asn	tgc Cys	caa Gln	2028
625 630 635																
ata Ile	cgt Arg	tcc Ser	aaa Lys	gga Gly	ttt Phe	tcc Ser	ata Ile	ttt Phe	cct Pro	gag Glu	gaa Glu	gat Asp	atg Met	ggg Gly	tca Ser	2076
640 645 650 655																
atc Ile	atg Met	gaa Glu	aga Arg	gca Ala	tct Ser	ggg Gly	aag Lys	act Thr	gaa Glu	aac Asn	acc Thr	tgg Trp	ctt Leu	cta Leu	ggg Gly	2124
660 665 670 675																
ttc Phe	ctc Leu	att Ile	gct Ala	ctt Leu	cct Pro	att Ile	ctc Leu	att Ile	gta Val	aca Thr	acc Thr	gca Ala	ata Ile	gtt Val	ttg Leu	2172
680 685 690 695																
gca Ala	agg Arg	aaa Lys	cag Gln	ttg Leu	aaa Lys	aac Asn	tgg Trp	ttc Phe	gcc Ala	aag Lys	gaa Glu	gag Glu	gaa Glu	ttc Phe	cca Pro	2220
700 705 710 715																
agt Ser	agc Ser	gaa Glu	tct Ser	aaa Lys</												

```

tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
720          725          730          735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
          740          745          750
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
          755          760          765
caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
Gln Ser Ser Ser Asn
          770
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Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
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Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
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Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
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Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
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Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
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1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Index**
 10. **Table of Contents**
 11. **Abstract**
 12. **Summary**
 13. **Key Words**
 14. **Keywords**
 15. **Subject Headings**
 16. **Classification**
 17. **Indexing**
 18. **Keywords**
 19. **Subject Headings**
 20. **Classification**
 21. **Indexing**
 22. **Keywords**
 23. **Subject Headings**
 24. **Classification**
 25. **Indexing**
 26. **Keywords**
 27. **Subject Headings**
 28. **Classification**
 29. **Indexing**
 30. **Keywords**
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 cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
 Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
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 Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
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 Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
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35 40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
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Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65 70 75 80
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 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 165 170 175
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 180 185 190
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 195 200 205 210
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
 215 220 225
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
 230 235

<210> 81
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..26

<220>
 <221> CDS
 <222> 27..689

<220>
 <221> 3'UTR
 <222> 690..1406

<220>
 <221> polyA_signal
 <222> 1302..1307

<220>
 <221> polyA_site
 <222> 1325..1406

<400> 81
 cccggaagtg cgcaggcgct ggcaag atg gcg gga ggg gtg cgc ccg ctg cgg 53
 Met Ala Gly Gly Val Arg Pro Leu Arg
 -30 -25
 ggc ctc cgc gcc ttg tgt cgc gtg ctg ctc ttc ctt tcg cag ttc tgc 101
 Gly Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys
 -20 -15 -10
 att ctg tcg ggc ggt gaa agt act gaa atc cca cct tat gtg atg aag 149
 Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys
 -5 1 5 10
 tgt ccg agc aat ggt ttg tgt agc agg ctt cct gca gac tgt ata gac 197
 Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp
 15 20 25
 tgc aca aca aat ttc tcc tgt acc tat ggg aag cct gtc act ttt gac 245

Cys	Thr	Thr	Asn	Phe	Ser	Cys	Thr	Tyr	Gly	Lys	Pro	Val	Thr	Phe	Asp		
			30					35					40				
tgt	gca	gtg	aaa	cca	tct	gtt	acc	tgt	gtt	gat	caa	gac	ttc	aaa	tcc	293	
Cys	Ala	Val	Lys	Pro	Ser	Val	Thr	Cys	Val	Asp	Gln	Asp	Phe	Lys	Ser		
			45				50					55					
caa	aag	aac	ttc	atc	att	aac	atg	act	tgc	aga	ttt	tgc	tgg	cag	ctt	341	
Gln	Lys	Asn	Phe	Ile	Ile	Asn	Met	Thr	Cys	Arg	Phe	Cys	Trp	Gln	Leu		
			60			65					70						
cct	gaa	aca	gat	tac	gag	tgt	acc	aac	tcc	acc	agc	tgc	atg	acg	gtg	389	
Pro	Glu	Thr	Asp	Tyr	Glu	Cys	Thr	Asn	Ser	Thr	Ser	Cys	Met	Thr	Val		
					80					85					90		
tcc	tgt	cct	cgg	cag	cgc	tac	cct	gcc	aac	tgc	acg	gtg	cgg	gac	cac	437	
Ser	Cys	Pro	Arg	Gln	Arg	Tyr	Pro	Ala	Asn	Cys	Thr	Val	Arg	Asp	His		
				95				100						105			
gtc	cac	tgc	ttg	ggt	aac	cgt	act	ttt	ccc	aaa	atg	cta	tat	tgc	aat	485	
Val	His	Cys	Leu	Gly	Asn	Arg	Thr	Phe	Pro	Lys	Met	Leu	Tyr	Cys	Asn		
			110					115				120					
tgg	act	gga	ggc	tat	aag	tgg	tct	acg	gct	ctg	gct	cta	agc	atc	acc	533	
Trp	Thr	Gly	Gly	Tyr	Lys	Trp	Ser	Thr	Ala	Leu	Ala	Leu	Ser	Ile	Thr		
			125				130				135						
ctc	ggt	ggg	ttt	gga	gca	gac	cgt	ttc	tac	ctg	ggc	cag	tgg	cgg	gaa	581	
Leu	Gly	Gly	Phe	Gly	Ala	Asp	Arg	Phe	Tyr	Leu	Gly	Gln	Trp	Arg	Glu		
			140			145					150						
ggc	ctc	ggc	aag	ctc	ttc	agc	ttc	ggt	ggc	ctg	gga	ata	tgg	acg	ctg	629	
Gly	Leu	Gly	Lys	Leu	Phe	Ser	Phe	Gly	Gly	Leu	Gly	Ile	Trp	Thr	Leu		
			155		160					165					170		
ata	gac	gtc	ctg	ctc	att	gga	gtt	ggc	tat	gtt	gga	cca	gca	gat	ggc	677	
Ile	Asp	Val	Leu	Leu	Ile	Gly	Val	Gly	Tyr	Val	Gly	Pro	Ala	Asp	Gly		
				175				180						185			
tct	ttg	tac	att	tagct	gtg	ggt	gtgtg	cttca	gaaagg	gagca	ggg	cttagaa				729	
Ser	Leu	Tyr	Ile														
			190														
aaagcccttt	tg	tc	gtagg				agttgat	gtg	gtgag	tga	tatat	tttcta	tg	ttttta	aat	789	
gtacacgcatc	tg	tact	tttgt			ttgc	cttgat	aa	aggta	aga	taaat	gaaac	gct	gaact	at	849	
gctaactctgg	aa	tttgt	tttt			tatt	tg	cctg	aa	tatat	tttt	ctgtga	aaaa	aattaa	aaa	909	
acgtacttaa	gcc	aggag	aaa			tga	aattata	c	agt	gattga	aat	ccattta	att	cctat	ga	969	
cttttgtttt	gt	attg	ccca			agt	caaa	acta	cat	cactt	gt	at	ctccag	cc	caa	atgtagt	1029
ctgccttgaa	aa	gt	cttt	ca		gct	gtg	actg	cag	gaag	tgg	gag	tgt	tttt	att	gttagct	1089
aattgctgtg	act	gc	cagg	aa		gt	ggg	ag	tgt			gg	cta	aatt	ga	agttattagg	1149
ctcagcttca	gt	cat	gt	gt													

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<210> 82
<211> 221
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> 1..32
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<400> 82
Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg
      -30                -25                -20
Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
      -15                -10                -5
Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
1      5                10                15
Ser Arg Leu Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys
      20                25                30

```

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
 35 40 45
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
 50 55 60
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
 65 70 75 80
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
 85 90 95
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
 100 105 110
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
 115 120 125
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
 130 135 140
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
 145 150 155 160
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
 165 170 175
 Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile
 180 185

<210> 83
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 83
 tccccggccg ccgcggttgc gtcgcccgcg ctgcgactga agcccggggc ctgcgcgcgc 60
 gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe

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<220>  
<221> SIGNAL  
<222> 1..24
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78

<210> 85
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 85
 tccccggccg ccgcggttgc gctcgcgcgcg ctgcactga agccccgggcc ctgcgcgcgc 60
 gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc gggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
 Met Leu Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct ccg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100 105
 ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550
 Gly Pro Ser
 acagacattc gggagacggc ctctgtgttc gccatcactg cggcgggcgc cagccacggc 610
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
 cgggccccctc cccggccctc cggcctgccc ggcacccccg gacccccctg ccccgcgggc 730
 tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
 gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
 gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
 accgagtgc aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
 ctgcctccat ttgcgaggt gggcgcgcg ctgctggagc gcttycacgg cgcctcacgc 1030
 gtcatgggca ccaacgacgg caaggccctg ctgcccgcg tccgcacgct caagccgcgc 1090

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ggccgagcgg acctcctcta cgcgcgcgat tcgcccgact tctgcgcccc caaccgacgc 1150
accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgctgcgg ccgcgggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgccctgtgcc gcttccactg gtgctgcgta gtacagtgcc accgctgcgg tgtgcgcaag 1330
gagctcagcc tctgcctgtg acccgccgcc cgcccgctag actgacttcg cgcagcggtg 1390
gctcgcacct gtgggacctc agggcaccgg caccggggcg ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gcccagggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg aactgtaca ggccctccct ccccttggcc tctaggagga aacagtttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
aaaa

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<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
                                -20                -15                -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
                                -5                1                5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
                                10                15                20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25                                30                35                40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
                                45                50                55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
                                60                65                70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
                                75                80                85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90                                95                100
Gly Pro Ser
105

```

```

<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..151

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<220>
<221> CDS
<222> 152..655

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<220>
<221> 3'UTR
<222> 656..1431

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<220>
<221> polyA_signal
<222> 1399..1404

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<220>

<221> polyA_site

<222> 1416..1431

<400> 87

aatttttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gccccaaacca agggccccag agaggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172

Met Leu Phe Arg Leu Ser Glu

1 5

cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly

10

15

20

gag ggg cac cat ctc aag tgc aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr

25

30

35

cca cct tgc ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln

tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu

ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu

gaa gag gag gat gat gaa gaa gag gaa gaa gag gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala

gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys

ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu

tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu

agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly

aca taggcacca gctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr

tccccagaaa ccactctat cctcaccctg ttttgtgctc ttcccctcgc ctgctagggc 765
tgcggttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccacctttt 825

ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccaccctgc cagtcattcc 885
tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc 945

gggaacaggg atttgccctt cacaattcta ctccccagat cctctccctt ggacacagga 1005
gacccacagg gcaggacct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065

cttagatcct tttctacca ctttctatg gaggattcca agtcaccact tctctaccg 1125
gcttctacca gggctccagga ctaaggcgtt tttctccata gcctcaacat tttgggaatc 1185

ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tggttgcttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305

acagcggggg gcgccagggt ttcttgtcc cccagctgct ctgccccttt ccccttcttc 1365
cctgactcca ggctgaacc cctcccgctg tgtaataaat ctttgtaaag aaaaaaaaaa 1425

aaaaaa 1431

<210> 88
<211> 168
<212> PRT
<213> Homo sapiens

<400> 88

Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser

```

1           5           10           15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
           20           25           30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
           35           40           45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
           50           55           60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65           70           75           80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
           85           90           95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
           100          105          110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
           115          120          125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
           130          135          140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145          150          155          160
Pro Ser Pro Ser Glu Pro Gly Thr
           165

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<210> 89
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

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<400> 89
aatTTTTtct cacaaggact gggTgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gcccaaacca agggccccag agaggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
Met Leu Phe Arg Leu Ser Glu
           1           5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
           10          15          20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
           25          30          35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
           40          45          50          55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364

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<210> 91
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..47

<220>
 <221> CDS
 <222> 48..1301

<220>
 <221> 3'UTR
 <222> 1302..1417

<220>
 <221> polyA_signal
 <222> 1360..1365

<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91
 ctctctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct 56
 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
 1 5 10
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
 15 20 25
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
 30 35 40
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
 45 50 55 60
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 65 70 75
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 80 85 90
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 95 100 105
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 110 115 120
 ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac 536
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 125 130 135 140
 tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa 584
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 145 150 155

10	15	20																	
Lys	Ile	Thr	Pro	Asn	Leu	Ala	Glu	Phe	Ala	Phe	Ser	Leu	Tyr	Arg	Gln				
25					30					35					40				
Leu	Ala	His	Gln	Ser	Asn	Ser	Thr	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser				
				45					50					55					
Ile	Ala	Thr	Ala	Phe	Ala	Met	Leu	Ser	Leu	Gly	Thr	Lys	Ala	Asp	Thr				
			60					65					70						
His	Asp	Glu	Ile	Leu	Glu	Ser	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro				
	75						80					85							
Glu	Ala	Gln	Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn				
	90					95					100								
Gln	Pro	Asp	Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu				
105				110						115					120				
Ser	Glu	Gly	Leu	Lys	Leu	Val	Asp	Lys	Phe	Leu	Glu	Asp	Val	Lys	Lys				
				125					130					135					
Leu	Tyr	His	Ser	Glu	Ala	Phe	Thr	Val	Asn	Phe	Gly	Asp	Thr	Glu	Glu				
			140					145					150						
Ala	Lys	Lys	Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys				
	155					160						165							
Ile	Val	Asp	Leu	Val	Lys	Glu	Leu	Asp	Arg	Asp	Thr	Val	Phe	Ala	Leu				
	170					175					180								
Val	Asn	Tyr	Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val				
185				190						195					200				
Lys	Asp	Thr	Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Ala	Thr	Thr	Val				
			205						210					215					
Lys	Val	Pro	Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys				
	220							225					230						
Lys	Lys	Leu	Ser	Ser	Trp	Val	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala					
	235						240					245							
Thr	Ala	Ile	Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu				
	250					255					260								
Asn	Glu	Leu	Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp				
265				270						275				280					
Arg	Arg	Ser	Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr				
			285						290					295					
Tyr	Asp	Leu	Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe				
	300						305					310							
Ser	Asn	Gly	Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys				
	315						320					325							
Leu	Ser	Lys	Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly				
	330					335					340								
Thr	Glu	Ala	Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile				
345				350						355				360					
Pro	Pro	Glu	Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Glu				
			365						370					375					
Gln	Asn	Thr	Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr				
	380						385					390							

Gln Lys

<210> 93
 <211> 1115
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..277

<220>
 <221> CDS
 <222> 278..733

<220>

<221> 3'UTR
<222> 734..1115

<220>
<221> polyA_signal
<222> 1072..1077

<220>
<221> polyA_site
<222> 1101..1115

<400> 93
ctctttgctc taacagacag cagcgacttt aggctggata atagtcaa atctttacctcg 60
ctcttttact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
Met His Phe Gly Leu Leu

-15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
-10 -5 1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5 10 15 20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
25 30 35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
40 45 50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55 60 65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70 75 80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85 90 95 100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
105 110 115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120 125 130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggg 783
Ala Ile
ccgaatgggt tccagggtgga taattatgga acccagctca atgctgtgaa taactocctg 843
actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaaac aaatgatggg 903
tggaagaatg cggctcatat ttaccaagtc tttctgaacg cctttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgcctatggt aatattttgtg cttttggcat 1023
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..19

<400> 94
 Met His Phe Gly Leu Leu Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 30 35 40 45
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys
 80 85 90
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr
 95 100 105
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser
 110 115 120 125
 Ser Met Val Asp Ala Trp Ala Ile
 130

<210> 95
 <211> 1307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..252

<220>
 <221> CDS
 <222> 253..744

<220>
 <221> 3'UTR
 <222> 745..1307

<220>
 <221> polyA_signal
 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1292..1307

<400> 95
 ctctttgctc taacagacag cagcgacttt aggctggata atagtcaa at tcttacctcg 60
 ctctttcact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac ttcatcaga 240
 gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala
 -25 -20 -15
 tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339
 Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp
 -10 -5 1
 tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca 387
 Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro
 5 10 15
 cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc 435

Asn Gln Gln Phe
135

<210> 97
<211> 1855
<212> DNA
<213> Homo sapiens

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<222> 1..117

<220>
<221> CDS
<222> 118..504

<220>
<221> 3'UTR
<222> 505..1855

<220>
<221> polyA_signal
<222> 1819..1824

<220>
<221> polyA_site
<222> 1840..1855

<400> 97
tccccggcgc cgcgcgttgc gctcgcgcgc ctcgcactga agccccgggcc ctcgcgcgcc 60
gcggttcgcc cgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct ccg ggc gcc ccg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100 105
gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
Ala
cctcccaggc ccctggggca gccctccgc cgcagggttc aggtcccagg cccagctga 614
ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
cgtgttcgcc atcactgcgg ccggcgccag ccaagccgtc acgcaggcct gttctatggg 734
cgagctgctg cagtgcggct gccaggcgcc ccgcggggcg gccctcccc gccctccgg 794
cctgcccggc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgcgcctg 854
ggagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914

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ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974
cgaggcgggc aggctggccg tgcggagcca cagcgcgacc gaggcgaaat gccacgggct 1034
gtcgggatca tgcgcgctgc gcacctgctg gcagaagctg cctccatttc gcgaggtggg 1094
cgcgcggtg ctggagcgtc tccacggcgc ctacgcgctc atgggcacca acgacggcaa 1154
ggccctgctg ccgcgcgtcc gcaagctcaa gccgcggggc cgagcggacc tcctctacgc 1214
cgccgattcg ccgcacttct gcgcccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
tcgcgcctgc aatagcagcg ccccggaact cagcggctgc gacctgctgt gctgcggccg 1334
cgggcaccgc caggagagcg tgcagctcga agagaactgc ctgtgccgct tccactggtg 1394
ctgcgtagta cagtgccacc gctgccgtgt gcgaaggag ctgagcctct gcctgtgacc 1454
cgccgcccgg ccgctagact gacttcgcgc agcgggtggc cgcacctgtg ggacctcagg 1514
gcaccggcac cgggcgcctc tcgcgcctgc agccagcct ctccctgcca aagcccaact 1574
cccagggtc tggaaatggt gaggcgaggg gcttgagagg aacgcccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgtc cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct aggaggaaac agtttttag actggaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaac tgctggccac aggatggtg gtgaggttag 1814
tatcaataaa gatatttaaa ccacaaaaaa aaaaaaaaaa a 1855

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<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
          10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
          75          80          85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
          90          95          100
Ala
105

```

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<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..94

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<220>
<221> CDS
<222> 95..613

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<220>
<221> 3'UTR
<222> 614..667

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65              70              75              80
His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
              85              90              95
Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
              100              105              110
Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
              115              120              125
Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser
              130              135              140
Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
145              150              155              160
Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
              165              170

```

```

<210> 101
<211> 1062
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..153

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<220>
<221> CDS
<222> 154..639

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<220>
<221> 3'UTR
<222> 640..1062

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<220>
<221> polyA_signal
<222> 1023..1028

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<220>
<221> polyA_site
<222> 1047..1062

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<400> 101
attggtgtat ggctttgcag caataactga tggctgtttc ccctcctgct ttatctttca 60
gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc 120
gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
              Met Ala Cys Trp Pro Gln Leu
              1              5
agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys
              10              15              20
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
              25              30              35
atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat 318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
              40              45              50              55
ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag 366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
              60              65              70
ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
              75              80              85
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
              90              95              100

```

```

cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac      510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp
    105                      110                      115
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc      558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
    120                      125                      130                      135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag      606
Lys Lys Ser Ser Arg Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
    140                      145                      150
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg      659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
    155                      160
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatat gccagatgg      719
cctgaagtaa ctgaagaatc acaaaagaag tgaaaaggcc ctgcctcgcc ttaactgatg      779
acgttccacc attgtgattt gttcctgccc caccttaact gagtgattaa ccctgtgaat      839
ttccttctcc tggctcagaa gctccccccac tgagcacctt gtgacccctt gcccctgccc      899
accagagaac aacccccctt gactgtaatt ttccattacc ttcccaaata ctataaaacg      959
gccccacccc tatctccctt tgetgactct cttttcggac tcagcccacc tgcagccagg      1019
tgaaaaaaac agcttttattg ctcacacaaa aaaaaaaaaa aaa                      1062

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<210> 102
 <211> 162
 <212> PRT
 <213> Homo sapiens

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<400> 102
Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Leu Trp Lys Asn Leu Thr
1      5      10      15
Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
    20      25      30
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
    35      40      45
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
    50      55      60
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
    65      70      75      80
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
    85      90      95
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
    100      105      110
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
    115      120      125
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
    130      135      140
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
    145      150      155      160
Leu Leu

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<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..149

<220>
 <221> CDS
 <222> 150..392

<220>
 <221> 3'UTR

<222> 393..933

<220>

<221> polyA_site

<222> 63..933

<400> 103

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aaaccctcag ggacctggtg tagacgcaga atctgtttca cacaacaact gctatttgaa 60
ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
cagatgtgta cggatgaaaa tacagtgtg atg agt cag aaa ccg gcc aag gag 173
                               Met Ser Gln Lys Pro Ala Lys Glu
                               1           5
ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
   10           15           20
cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
   25           30           35           40
gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
           45           50           55
gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
           60           65           70
aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
Lys Ile Arg Pro Thr Pro Lys Lys Lys
           75           80
ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472
agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
gctcatgggtc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
tcattccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
tggaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
gcgtgggtggc gggcgccctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
gaacctggga ggcggagctt gcagtgcgc gagatcgcac cactgcactc cagcctgggc 892
gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933
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<210> 104

<211> 81

<212> PRT

<213> Homo sapiens

<400> 104

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Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
1           5           10           15
Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
   20           25           30
Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
   35           40           45
Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
   50           55           60
Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
   65           70           75           80
Lys
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<210> 105

<211> 1187

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..34

Ser	Lys	Glu	Lys	Gly	Leu	Thr	Lys	Lys	Arg	Thr	Lys	Val	Gln	Lys	Lys	
tca	ctg	ctt	ctc	aag	aaa	ccc	ctt	cgg	gtt	gac	ctc	atc	ctc	gag	aac	387
Ser	Leu	Leu	Leu	Lys	Lys	Pro	Leu	Arg	Val	Asp	Leu	Ile	Leu	Glu	Asn	
aca	tcc	aaa	gtc	cct	gcc	ccc	aaa	gac	gtc	ctc	gcc	cac	cag	gtc	ccc	435
Thr	Ser	Lys	Val	Pro	Ala	Pro	Lys	Asp	Val	Leu	Ala	His	Gln	Val	Pro	
125					130					135					140	
aac	gcc	aag	aag	ctc	agg	cgg	aag	gag	cag	cta	tgg	gag	aag	ctg	gcc	483
Asn	Ala	Lys	Lys	Leu	Arg	Arg	Lys	Glu	Gln	Leu	Trp	Glu	Lys	Leu	Ala	
aag	cag	ggc	gag	ctg	ccc	cgg	gag	gtg	cgc	agg	gcc	cag	gcc	cgg	ctc	531
Lys	Gln	Gly	Glu	Leu	Pro	Arg	Glu	Val	Arg	Arg	Ala	Gln	Ala	Arg	Leu	
ctc	aac	cct	tct	gca	aca	agg	gcc	aag	ccc	ggg	ccc	cag	gac	acc	gta	579
Leu	Asn	Pro	Ser	Ala	Thr	Arg	Ala	Lys	Pro	Gly	Pro	Gln	Asp	Thr	Val	
gag	cgg	ccc	ttc	tac	gac	ctc	tgg	gcc	tca	gac	aac	ccc	ctg	gac	agg	627
Glu	Arg	Pro	Phe	Tyr	Asp	Leu	Trp	Ala	Ser	Asp	Asn	Pro	Leu	Asp	Arg	
ccg	ttg	gtt	ggc	cag	gat	gag	ttt	ttc	ctg	gag	cag	acc	aag	aag	aaa	675
Pro	Leu	Val	Gly	Gln	Asp	Glu	Phe	Phe	Leu	Glu	Gln	Thr	Lys	Lys	Lys	
205					210					215					220	
gga	gtg	aag	cgg	cca	gca	cgc	ctg	cac	acc	aag	ccg	tcc	cag	gca	ccc	723
Gly	Val	Lys	Arg	Pro	Ala	Arg	Leu	His	Thr	Lys	Pro	Ser	Gln	Ala	Pro	
gcc	gtg	gag	gtg	gcg	cct	gcc	gga	gct	tcc	tac	aat	cca	tcc	ttt	gaa	771
Ala	Val	Glu	Val	Ala	Pro	Ala	Gly	Ala	Ser	Tyr	Asn	Pro	Ser	Phe	Glu	
gac	cac	cag	acc	ctg	ctc	tca	gcg	gcc	cac	gag	gtg	gag	ttg	cag	cgg	819
Asp	His	Gln	Thr	Leu	Leu	Ser	Ala	Ala	His	Glu	Val	Glu	Leu	Gln	Arg	
cag	aag	gag	gcg	gag	aag	ctg	gag	cgg	cag	ctg	gcc	ctg	ccc	gcc	acg	867
Gln	Lys	Glu	Ala	Glu	Lys	Leu	Glu	Arg	Gln	Leu	Ala	Leu	Pro	Ala	Thr	
gag	cag	gcc	gcc	acc	cag	gag	tcc	aca	ttc	cag	gag	ctg	tgc	gag	ggg	915
Glu	Gln	Ala	Ala	Thr	Gln	Gln	Ser	Thr	Phe	Gln	Glu	Leu	Cys	Glu	Gly	
285					290					295					300	
ctg	ctg	gag	gag	tcg	gat	ggg	gag	ggg	gag	cca	ggc	cag	ggc	gag	ggg	963
Leu	Leu	Glu	Glu	Ser	Asp	Gly	Glu	Gly	Glu	Pro	Gly	Gln	Gly	Glu	Gly	
ccg	gag	gct	ggg	gat	gcc	gag	gtc	tgt	ccc	acg	ccc	gcc	cgc	ctg	gcc	1011
Pro	Glu	Ala	Gly	Asp	Ala	Glu	Val	Cys	Pro	Thr	Pro	Ala	Arg	Leu	Ala	
acc	aca	gag	aag	aag	acg	gag	cag	cag	cgg	cgg	cgg	gag	aag	gct	gtg	1059
Thr	Thr	Glu	Lys	Lys	Thr	Glu	Gln	Gln	Arg	Arg	Arg	Glu	Lys	Ala	Val	
cac	agg	ctg	cgg	gta	cag	cag	gcc	gcg	ttg	cgg	gcc	gcc	cgg	ctc	cgg	1107
His	Arg	Leu	Arg	Val	Gln	Gln	Ala	Ala	Leu	Arg	Ala	Ala	Arg	Leu	Arg	
His	Gln	Glu	Leu	Phe	Arg	Leu	Arg	Gly	Ile	Lys	Ala	Gln	Val	Ala	Leu	1155
agg	ctg	gcg														

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Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser
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ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa 1395
Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys
  445                      450                      455                      460
cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc 1443
Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile
                      465                      470                      475
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Gln Leu
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<213> Homo sapiens

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  35          40          45
Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
  50          55          60
Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
  65          70          75          80
Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
  85          90          95
Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
  100         105         110
Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
  115         120         125
Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
  130         135         140
Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu
  145         150         155         160
Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser
  165         170         175
Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe
  180         185         190
Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly
  195         200         205
Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg
  210         215         220
Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val
  225         230         235         240
Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr
  245         250         255
Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala
  260         265         270
Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala
  275         280         285
Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu
  290         295         300
Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly
  305         310         315         320
Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys
  325         330         335
Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg
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1789

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 <212> PRT
 <213> Homo sapiens

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 Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
 20 25 30
 Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
 35 40 45
 Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
 50 55 60 65
 Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
 70 75 80
 Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
 85 90 95
 Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
 100 105 110
 Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
 115 120 125
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
 130 135 140 145
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
 150 155 160
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
 165 170 175
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
 180 185 190
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
 195 200 205
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
 210 215 220 225
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
 230 235 240
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
 245 250 255
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
 260 265 270
 Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
 275 280 285
 Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
 290 295 300 305
 Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
 310 315 320
 Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
 325 330 335
 Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
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 Asp Leu
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 Met Ser Thr Phe
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 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
 5 10 15 20
 ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210
 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser
 25 30 35
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu
 40 45 50
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
 55 60 65
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
 70 75 80
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys
 85 90 95 100
 tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450
 Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu
 105 110 115
 aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498
 Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu
 120 125 130
 tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546
 Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala
 135 140 145
 tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
 150 155 160
 atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt 642
 Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu
 165 170 175 180

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Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn	Phe	Phe	Gly	Thr	
				185					190				195			
gtg	gag	gtc	aca	aag	acg	ttt	ttg	cct	ctt	ctt	aga	aaa	tcc	aaa	ggg	738
Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg	Lys	Ser	Lys	Gly	
				200					205				210			
agg	ctg	gtg	aat	gtc	agc	agc	atg	gga	gga	ggg	gcc	cca	gtg	gaa	agg	786
Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala	Pro	Val	Glu	Arg	
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ctg	gca	tct	tat	ggc	tca	tca	aag	gcg	gct	gtg	acc	atg	ttc	tca	tca	834
Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr	Met	Phe	Ser	Ser	
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Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys	Val	Ala	Ser	Ile	
				245					250				255			
caa	cct	gga	ggc	ttc	cta	aca	aat	atc	gca	ggc	acc	agt	gac	aag	tgg	930
Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr	Ser	Asp	Lys	Trp	
				265					270				275			
gaa	aag	ctg	gag	aag	gac	att	ctg	gac	cac	ctc	ccc	gct	gag	gta	cag	978
Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro	Ala	Glu	Val	Gln	
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gaa	gac	tac	tgc	cag	gac	tac	atc	tta	gca	cag	cgg	aat	ttc	ctc	cta	1026
Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg	Asn	Phe	Leu	Leu	
				295					300				305			
ttg	atc	aac	tgc	tta	gcc	agc	aag	gac	ttc	tct	ccg	gtg	ctg	cgg	gac	1074
Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro	Val	Leu	Arg	Asp	
				310					315				320			
atc	cag	cat	gct	atc	ttg	gcg	aag	agc	cct	ttt	gcc	tat	tac	acg	cca	1122
Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala	Tyr	Tyr	Thr	Pro	
				325					330				335			
ggg	aaa	ggc	gct	tac	ttg	tgg	atc	tgc	ctt	gct	cac	tat	ttg	cct	att	1170
Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His	Tyr	Leu	Pro	Ile	
				345					350				355			
ggc	ata	tat	gat	tac	ttt	gct	aaa	aga	cat	ttt	ggc	caa	gac	aag	ccc	1218
Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly	Gln	Asp	Lys	Pro	
				360					365				370			
atg	ccc	aga	gct	tta	aga	atg	cct	aac	tac	aag	aaa	aag	gcc	ccc		1263
Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys	Lys	Ala	Pro		
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<211> 387

<212> PRT

<213> Homo sapiens

<400> 112

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			20					25					30		
Gln	Leu	Trp	Ser	Trp	Met	Val	Cys	Leu	Ala	Gly	Leu	Cys	Ala	Val	Cys
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Leu	Leu	Ile	Leu	Ser	Pro	Phe	Trp	Gly	Leu	Ile	Leu	Phe	Ser	Val	Ser
	50					55					60				
Cys	Phe	Leu	Met	Tyr	Thr	Tyr	Leu	Ser	Gly	Gln	Glu	Leu	Leu	Pro	Val
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Asp	Gln	Lys	Ala	Val	Leu	Val	Thr	Gly	Gly	Asp	Cys	Gly	Leu	Gly	His
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Ala	Leu	Cys	Lys	Tyr	Leu	Asp	Glu	Leu	Gly	Phe	Thr	Val	Phe	Ala	Gly
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Gly	Glu	Leu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn	
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Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg	
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Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala	
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Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr	
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Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys	
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Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr	
			260					265					270			
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro	
		275					280					285				
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg	
		290				295					300					
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro	
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Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala	
				325					330						335	
Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His	
			340					345						350		
Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly	
		355					360					365				
Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys	
		370				375					380					
Lys	Ala	Pro														
385																